

## Cartographic Representation of Averaged Pairwise Information (CRAPI): a new exploratory tool to investigate spatial structures illustrated with genetic data from the *Watermelon mosaic virus*

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Dedicated analyses in landscape genetics require *a priori* knowledge on species dispersal abilities. When little is known about the species under study these methods are difficult to apply and, therefore, we rely on exploratory approaches allowing to visualize and confront genetic and environmental variation patterns. We developed a novel exploratory method, free from assumptions, to investigate spatial variations in pairwise genetic metrics computed between georeferenced samples. Graphical outputs can be mapped on landscape layers to further explore potential relationships between genetic and environmental structures. The method relies on both a spatial grid and a network for which the links are materialized by ellipsoidal polygons bearing the pairwise metric values computed between samples. The network is overlayed on the spatial grid and a given cell receives the weighted mean of all ellipses values intersecting a top this cell. CRAPI includes a randomization procedure to test the relevance of the spatial structure emerging from the analysis. To illustrate our method we analysed 396 sequences of native and invasive strains of the Watermelon mosaic virus obtained from cucurbits collected between 2004 and 2008 in South Eastern France. The CRAPI analyses allowed to visualize both the contact zone between native and invasive strains, arising during the early stage of the invasion, and potential effects of landscape features on virus dissemination.